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     (FILE 'HOME' ENTERED AT 14:37:24 ON 15 JAN 2003)

     INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
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              3    FILE BIOSIS
              3    FILE BIOTECHNO
              1    FILE CABA
              7    FILE CAPLUS
              2    FILE EMBASE
              3    FILE ESBIOBASE
              1    FILE FEDRIP
              1    FILE FSTA
              2    FILE GENBANK
              3    FILE LIFESCI
              4    FILE MEDLINE
              1    FILE PROMT
              3    FILE SCISEARCH
              1    FILE TOXCENTER
              3    FILE USPATFULL
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              2    FILE ADISINSIGHT
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             33    FILE ANABSTR
             23    FILE AQUASCI
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             19    FILE BIOCOMMERCE
           2452    FILE BIOSIS
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            427    FILE BIOTECHDS
           2325    FILE BIOTECHNO
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            555    FILE CANCERLIT
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             15    FILE CEN
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              3    FILE CROPU
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            129    FILE DRUGB
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             42    FILE DRUGU
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             59    FILE FROSTI
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              237   FILE WPINDEX
L2               QUE GLYCOSYLTRANSFERASE
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L5             8 DUP REM L4 (14 DUPLICATES REMOVED)
L6             0 S L1 AND LIPID
L7             1 S L1 AND DIACYLGLYCEROL

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=> d l5 ibib ab 1-8

L5 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:617911 CAPLUS
TITLE: Mechanism-based inhibitors of chitin synthase
AUTHOR(S): Yeager, Adam R.; Finney, Nathaniel S.
CORPORATE SOURCE: Department of Chemistry, University of California-San Diego, La Jolla, CA, 92093, USA
SOURCE: Abstracts of Papers, 224th ACS National Meeting, Boston, MA, United States, August 18-22, 2002 (2002), MEDI-057. American Chemical Society: Washington, D. C.
CODEN: 69CZPZ
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB Fungi rely on the enzyme chitin synthase (CS) to produce chitin (poly-N-acetylglucosamine, GlcNAc), an essential cell wall component involved in cellular reprodn. The enzyme polymerizes long chains of chitin utilizing an activated donor substrate, UDP-GlcNAc. The native structure of chitin has a screw-axis in which each GlcNAc monomer is rotated 180 degrees relative to the adjacent GlcNAc in the chain. Similar to other **processive glycosyltransferases** (cellulose and hyaluronan synthases), CS is membrane bound, few structural data exist, and little is known about its mechanism and how the enzyme accounts for the twist in the final structure. The weak affinity CS has for UDP-GlcNAc has precluded successful substrate-based inhibitors. We hope to exploit and demonstrate a previously proposed mechanism of action, in which two units of GlcNAc are added simultaneously or sequentially by two active sites. Preliminary results of a series of dimeric inhibitors will be presented.

L5 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
ACCESSION NUMBER: 2001:675533 CAPLUS
DOCUMENT NUMBER: 136:243579
TITLE: .beta.-D-glycan synthases and the CesA gene family: lessons to be learned from the mixed-linkage (1.fwdarw.3),(1.fwdarw.4).beta.-D-glucan synthase
AUTHOR(S): Vergara, Claudia E.; Carpita, Nicholas C.
CORPORATE SOURCE: Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN, 47907-1155, USA
SOURCE: Plant Molecular Biology (2001), 47(1-2), 145-160
CODEN: PMBIDB; ISSN: 0167-4412
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Cellulose synthase genes (CesAs) encode a broad range of **processive glycosyltransferases** that synthesize (1.fwdarw.4).beta.-D-glycosyl units. The proteins predicted to be encoded by these genes contain up to eight membrane-spanning domains and four "U-motifs" with conserved aspartate residues and a QxxRW motif that are essential for substrate binding and catalysis. In higher plants, the domain structure includes two plant-specific regions, one that is relatively conserved and a second, so-called "hypervariable region" (HVR). Anal. of the phylogenetic relationships among members of the CesA multi-gene families from two grass species, Oryza sativa and Zea mays, with Arabidopsis thaliana and other dicotyledonous species reveals that the CesA genes cluster into several distinct sub-classes. Whereas some sub-classes are populated by CesAs from all species, two sub-classes are populated solely by CesAs from grass species. The sub-class identity is primarily defined by the HVR, and the sequence in this region does not vary substantially among members of the same sub-class. Hence, we suggest that the region is more aptly termed a "class-specific region" (CSR). Several motifs contg. cysteine, basic, acidic and arom. residues indicate

that the CSR may function in substrate binding specificity and catalysis. Similar motifs are conserved in bacterial cellulose synthases, the Dictyostelium discoideum cellulose synthase, and other **processive glycosyltransferases** involved in the synthesis of non-cellulosic polymers with (1.fwdarw.4).beta.-linked backbones, including chitin, heparan, and hyaluronan. These analyses re-open the question whether all the CesA genes encode cellulose synthases or whether some of the sub-class members may encode other non-cellulosic (1.fwdarw.4).beta.-glycan synthases in plants. For example, the mixed-linkage (1.fwdarw.3)(1.fwdarw.4).beta.-D-glucan synthase is found specifically in grasses and possesses many features more similar to those of cellulose synthase than to those of other .beta.-linked crosslinking glycans. In this respect, the enzymic properties of the mixed-linkage .beta.-glucan synthases not only provide special insight into the mechanisms of (1.fwdarw.4).beta.-glycan synthesis but may also uncover the genes that encode the synthases themselves.

REFERENCE COUNT: 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 8 MEDLINE
ACCESSION NUMBER: 2001483417 MEDLINE
DOCUMENT NUMBER: 21114519 PubMed ID: 11178255
TITLE: Higher plant cellulose synthases.
AUTHOR: Richmond T
CORPORATE SOURCE: Department of Plant Biology, Carnegie Institution of Washington, 260 Panama Street, Stanford, CA 94305, USA.. todd@andrew2.stanford.edu
SOURCE: GENOMEBIOLOGY.COM, (2000) 1 (4) REVIEWS3001. Ref: 12
Journal code: 100960660. ISSN: 1465-6914.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20030105
Entered Medline: 20010830

AB SUMMARY: Cellulose, an aggregate of unbranched polymers of beta-1,4-linked glucose residues, is the major component of wood and thus paper, and is synthesized by plants, most algae, some bacteria and fungi, and even some animals. The genes that synthesize cellulose in higher plants differ greatly from the well-characterized genes found in Acetobacter and Agrobacterium sp. More correctly designated as 'cellulose synthase catalytic subunits', plant cellulose synthase (CesA) proteins are integral membrane proteins, approximately 1,000 amino acids in length. The sequences for more than 20 full-length CesA genes are available, and they show high similarity to one another across the entire length of the encoded protein, except for two small regions of variability. There are a number of highly conserved residues, including several motifs shown to be necessary for **processive glycosyltransferase** activity.
No crystal structure is known for cellulose synthase proteins, and the exact enzymatic mechanism is unknown. There are a number of mutations in cellulose synthase genes in the model organism Arabidopsis thaliana. Some of these mutants show altered morphology due to the lack of a properly developed primary or secondary cell wall. Others show resistance to well-characterized cellulose biosynthesis inhibitors.

L5 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:327912 CAPLUS
TITLE: From sequence to function: The challenge of characterizing putative glycosyltransferase genes in Arabidopsis.

AUTHOR(S): Richmond, Todd
CORPORATE SOURCE: Carnegie Institution of Washington, Stanford, CA, 94305, USA
SOURCE: Book of Abstracts, 219th ACS National Meeting, San Francisco, CA, March 26-30, 2000 (2000), CELL-054. American Chemical Society: Washington, D. C. CODEN: 69CLAC
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB The effort to sequence the entire Arabidopsis genome has proven to be a treasure trove for plant mol. biologists and cell wall researchers. A large superfamily of cellulose synthase (CesA) and cellulose synthase-like (Csl) genes has been identified in Arabidopsis, consisting of at least six subfamilies and over forty different genes. Homologs of many of these genes have been found in a wide variety of plant species, from mosses to trees. Sequence anal. indicates that these genes have conserved protein domains found in **processive glycosyltransferases**. Our lab. is taking a reverse genetic approach to detg. the function of several of these families of putative glycosyltransferases. I will discuss our progress in answering four important questions: where and when are these genes expressed, what is their enzymic function, and what is their importance in the biosynthesis of the plant cell wall.

L5 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:327861 CAPLUS
TITLE: Structure-function characterization of cellulose synthase.
AUTHOR(S): Saxena, Inder M.; Brown, R. Malcolm; Dandekar, Thomas
CORPORATE SOURCE: Section of Molecular Genetics and Microbiology, School of Biological Sciences, University of Texas, Austin, TX, 78712, USA
SOURCE: Book of Abstracts, 219th ACS National Meeting, San Francisco, CA, March 26-30, 2000 (2000), CELL-003. American Chemical Society: Washington, D. C. CODEN: 69CLAC
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB We have analyzed the globular region of cellulose synthase from Acetobacter xylinum by site-directed mutagenesis and motif anal., and obtained a structural model of this region using the genetic algorithm. Mutagenesis data confirmed that the conserved residues are essential for enzyme activity. The predicted structure of the catalytic region reveals the presence of a central elongated cavity between the conserved aspartic acid residues. The dimension of the cavity suggests that it can accommodate two UDP-glucose residues. The QXXRW motif is predicted to be involved in the binding of the growing glucan chain and residues in this motif are shown to be present in a region close to the central cavity. A similar structure was also obtained for the globular region of cellulose synthase from cotton. Based on our anal. of the globular region of cellulose synthase we have proposed a general model for the structure and action of **processive glycosyltransferases**.

L5 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:626343 CAPLUS
DOCUMENT NUMBER: 131:254319
TITLE: **Processive glycosyltransferases** of Bacillus and Staphylococcus and their use in glycolipid synthesis
INVENTOR(S): Wolter, Frank P.; Jorasch, Petra; Heinz, Ernst; Zahringer, Ulrich
PATENT ASSIGNEE(S): GVS Gesellschaft fur Erwerb und Verwertung Landwirtschaftlicher Pflanzensort, Germany; Forschungszentrum Borstel
SOURCE: PCT Int. Appl., 37 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9949052	A2	19990930	WO 1999-DE857	19990325
WO 9949052	A3	20000302		
W: AU, CA, CZ, HU, PL, SI, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
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CA 2329898	AA	19990930	CA 1999-2329898	19990325
AU 9941301	A1	19991018	AU 1999-41301	19990325
EP 1066388	A2	20010110	EP 1999-924670	19990325
R: AT, BE, CH, DE, DK, FR, GB, LI, NL, SE, IE				

PRIORITY APPLN. INFO.: DE 1998-19813017 A 19980325
DE 1998-19819958 A 19980505
WO 1999-DE857 W 19990325

AB The title enzymes and their use are disclosed. Thus, the ypfP gene of B. subtilis and of S. aureus were expressed in Escherichia coli. Both enzymes utilized UDP-glucose, and catalyzed addn. of up to 4 glucosyl moieties in .beta.(1.fwdarw.6) linkage to the substrates. The Bacillus enzyme used diacylglycerol, monoglucosyl diacylglycerol, diglucosyl diacylglycerol and alkyl-.alpha./.beta.-D-glucopyranosides as acceptor. The Staphylococcus enzyme could also use sterols and sterylglucosids as acceptors. Two novel phosphoglycolipids were identified.

L5 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 2
ACCESSION NUMBER: 1999:173455 CAPLUS
DOCUMENT NUMBER: 130:309111
TITLE: Chitin Oligosaccharide Synthesis by Rhizobia and Zebrafish Embryos Starts by Glycosyl Transfer to O4 of the Reducing-Terminal Residue
AUTHOR(S): Kamst, Eric; Bakkers, Jeroen; Quaedvlieg, Nicolette E. M.; Pilling, Jens; Kijne, Jan W.; Lugtenberg, Ben J. J.; Spaink, Herman P.
CORPORATE SOURCE: Clusius Laboratory, Institute of Molecular Plant Sciences, Leiden University, Leiden, 2333 AL, Neth.
SOURCE: Biochemistry (1999), 38(13), 4045-4052
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Lipochitin oligosaccharides are organogenesis-inducing signal mols. produced by rhizobia to establish the formation of nitrogen-fixing root nodules in leguminous plants. Chitin oligosaccharide biosynthesis by the Mesorhizobium loti nodulation protein NodC was studied in vitro using membrane fractions of an Escherichia coli strain expressing the cloned M. loti nodC gene. The results indicate that prenylpyrophosphate-linked intermediates are not involved in the chitin oligosaccharide synthesis pathway. It was obsd. that, in addn. to N-acetylglucosamine (GlcNAc) from UDP-GlcNAc, NodC also directly incorporates free GlcNAc into chitin oligosaccharides. Further anal. showed that free GlcNAc is used as a primer that is elongated at the nonreducing terminus. The synthetic glycoside p-nitrophenyl-.beta.-N-acetylglucosaminide (pNPGlcNAc) has a free hydroxyl group at C4 but not at C1 and could also be used as an acceptor by NodC, confirming that chain elongation by NodC takes place at the nonreducing-terminal residue. The use of artificial glycosyl acceptors such as pNPGlcNAc has not previously been described for a **processive glycosyltransferase**. Using this method, it was also shown that also the DG42-directed chitin oligosaccharide synthase

activity, present in exts. of zebrafish embryos, is able to initiate chitin oligosaccharide synthesis on pNPGlcNAc. Consequently, chain elongation in chitin oligosaccharide synthesis by M. loti NodC and zebrafish DG42 occurs by the transfer of GlcNAc residues from UDP-GlcNAc to O4 of the nonreducing-terminal residue, in contrast to earlier models on the mechanism of **processive** .beta.-glycosyltransferase reactions.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 3

ACCESSION NUMBER: 1997:566593 CAPLUS
DOCUMENT NUMBER: 127:244516
TITLE: Parallel-up structure evidences the molecular directionality during biosynthesis of bacterial cellulose
AUTHOR(S): Koyama, Makiko; Helbert, William; Imai, Tomoya; Sugiyama, Junji; Henrissat, Bernard
CORPORATE SOURCE: Wood Research Institute, Kyoto University, Kyoto, 611, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1997), 94(17), 9091-9095
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The "parallel-up" packing in cellulose I.alpha. and I.beta. unit cells was exptl. demonstrated by a combination of direct-staining the reducing ends of cellulose chains and microdiffraction-tilting electron crystallog. anal. Microdiffraction investigation of nascent bacterial cellulose microfibrils showed that the reducing end of the growing cellulose chains points away from the bacterium, and this provides direct evidence that polymn. by the cellulose synthase takes place at the nonreducing end of the growing cellulose chains. This mechanism is likely to be valid also for a no. of **processive glycosyltransferases** such as chitin synthases, hyaluronan synthases, and proteins involved in the synthesis of nodulation factor backbones.

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F4	3201	JICST-EPLUS
F5	2614	SCISEARCH
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F7	2325	BIOTECHNO
F8	2322	MEDLINE
F9	1969	ESBIOBASE
F10	1428	GENBANK
F11	1291	DGENE
F12	844	USPATFULL
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F19	427	BIOTECHDS
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F35          32   DDFU
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F43           4   NIOSHTIC
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     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
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L2                 QUE GLYCOSYLTRANSFERASE
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     FILE 'PASCAL, CAPLUS, EMBASE, JICST-EPLUS, SCISEARCH, BIOSIS, MEDLINE,
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L4              22 S L1 AND PROCESSIVE
L5               8 DUP REM L4 (14 DUPLICATES REMOVED)
L6               0 S L1 AND LIPID
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L7            1 L1 AND DIACYLGLYCEROL

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L7   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         1999:626343  CAPLUS
DOCUMENT NUMBER:          131:254319
TITLE:                    Processive glycosyltransferases of
                          Bacillus and Staphylococcus and their use in
                          glycolipid synthesis
INVENTOR(S):              Wolter, Frank P.; Jorasch, Petra; Heinz, Ernst;
                          Zahringer, Ulrich
PATENT ASSIGNEE(S):       GVS Gesellschaft fur Erwerb und Verwertung
                          Landwirtschaftlicher Pflanzensort, Germany;
                          Forschungszentrum Borstel
SOURCE:                   PCT Int. Appl., 37 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 German
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

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     CA 2329898         AA   19990930       CA 1999-2329898  19990325
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     EP 1066388         A2   20010110       EP 1999-924670   19990325
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PRIORITY APPLN. INFO.:                  DE 1998-19813017 A  19980325
                                        DE 1998-19819958 A  19980505
                                        WO 1999-DE857    W  19990325
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AB The title enzymes and their use are disclosed. Thus, the ypfP gene of B. subtilis and of S. aureus were expressed in Escherichia coli. Both enzymes utilized UDP-glucose, and catalyzed addn. of up to 4 glucosyl moieties in .beta.(1.fwdarw.6) linkage to the substrates. The Bacillus enzyme used **diacylglycerol**, monoglucosyl **diacylglycerol**, diglucosyl **diacylglycerol** and alkyl-.alpha./.beta.-D-glucopyranosides as acceptor. The Staphylococcus enzyme could also use sterols and sterylglucosids as acceptors. Two novel phosphoglycolipids were identified.